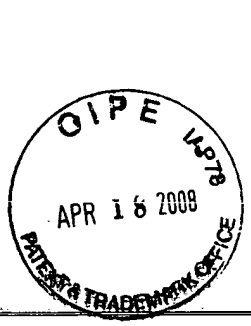

PATENT
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Hui Wang	Confirmation No.:	2131
Serial No.:	10/668,749	Art Unit:	1631
Filed:	September 23, 2003	Examiner:	Lori A. Clow
Customer No.:	21559		
Title:	METHODS AND SYSTEMS FOR NANOPORE DATA ANALYSIS		

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REPLY TO FINAL OFFICE ACTION

In reply to the final Office action that was mailed in connection with the above-captioned patent application on October 16, 2007, Applicant submits the following Remarks.

Claims 1, 4-11, 13, 15, 18-20, 36, and 37 are pending and stand rejected for lack of enablement. The basis of the rejection is that the step "analyzing the distribution of the non-target polynucleotide data points" is now optional in independent claims 1 and 15, yet the Examiner asserts this step is required when determining length diversity among polynucleotides in a sample. Applicant traverses the rejection.

Initially, independent claim 15 is directed to a system for performing nanopore data analysis that is operative to determine at least one of four alternatives. Only one of these alternatives, determining length diversity, requires analysis of the distribution of non-target polynucleotide data points. The second alternative is directed to determining length diversity, with the claim reciting:

> (ii) length diversity among polynucleotides present in a sample, wherein the distribution pattern includes at least one data cluster, and **wherein the nanopore data analysis system is operative to: analyze the distribution of non-target polynucleotide data points outside of the at least one cluster that indicates that non-target polynucleotides have a different length than the target polynucleotides**

Thus, the claim *explicitly requires* that a system used to determine length diversity be operative to analyze the distribution of non-target polynucleotide data points. That is, in contrast to the assertion by the Office, the ability to analyze non-target polynucleotide data points is not optional when determining length diversity in claim 15.

Similar to claim 15, claim 1 is directed to a method of performing nanopore data analysis that determines at least one of four alternatives. Again, only one of these four alternatives, determining length diversity, requires analysis of the distribution of non-target polynucleotide data points. Accordingly, the step of analyzing the distribution of non-target polynucleotide data points is optional to the method in the sense that three of the four alternatives do not require such a step. That is, one practicing alternatives (i), (iii), and (iv) need not analyze the distribution of non-target polynucleotide data points, and there is no reason to require this step for all embodiments of claim 1. Furthermore, alternative (ii) of claim 1 recites:

(ii) length diversity among polynucleotides present in a sample, wherein **distribution of non-target polynucleotide data points** outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides

This step positively recites use of the distribution of non-target polynucleotide data points. Thus, the "optional" step *must be performed* to carry out alternative (ii).

Finally, applicant notes that all claims have been rejected for lack of enablement based on the assertion that the independent claims do not require analysis of the distribution of non-target polynucleotide data points. As stated above, this step need not be employed with alternatives (i), (iii), or (iv). Claims 4-9 and 18, 19, and 36 are directed to these embodiments that do not require such an analysis; thus, there is no basis for the rejection of these claims. Claim 10 recites "said method comprising analyzing the distribution of the non-target polynucleotide data points." Thus, it cannot be said that this claim or its dependent claims 11 and 13 do not require such an analysis, and there is no basis for the rejection of these claims.

The rejection should be withdrawn.